

SEQUENCE LISTING

<110> Michael S.C. Fung
Bill N.C. Sun
Cecily R.Y. Sun

<120> Inhibitors of Complement Activation

<130> 98-2A

<150> 60/075,328

<151> 1998-02-20

<150> 09/253,689

<151> 1999-02-20

<160> 15

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 699

<212> DNA

<213> human

<220>

<221> CDS

<222> (4)...(687)

<400> 1

cg g atc ctg ggc ggc aga gag gcc gag gcg cac gcg cgg ccc tac atg 48

Ile-Leu Gly Gly Arg Glu Ala Glu Ala His Ala Arg Pro Tyr Met

1 5 10 15

gcg tcg gtg cag ctg aac ggc gcg cac ctg tgc ggc ggc gtc ctg gtg 96

Ala Ser Val Gln Leu Asn Gly Ala His Leu Cys Gly Gly Val Leu Val

20 25 30

gcg gag cag tgg gtg ctg agc gcg gcg cac tgc ctg gag gac gcg gcc 144

Ala Glu Gln Trp Val Leu Ser Ala Ala His Cys Leu Glu Asp Ala Ala

35 40 45

gac ggg aag gtg cag gtt ctc ctg ggc gcg cac tcc ctg tcg cag ccg 192

Asp Gly Lys Val Gln Val Leu Leu Gly Ala His Ser Leu Ser Gln Pro

50 55 60

gag ccc tcc aag cgc ctg tac gag gtg ctc cgc gca gtg ccc cac ccg 240

Glu Pro Ser Lys Arg Leu Tyr Asp Val Leu Arg Ala Val Pro His Pro

65 70 75

gac agc cag ccc gac acc atc gag cac gag ctc ctg ctg cta cag ctg 288

Asp Ser Gln Pro Asp Thr Ile Asp His Asp Leu Leu Leu Gln Leu

80 85 90 95

tcg gag aag gcc aca ctg ggc cct gct gtg cgc ccc ctg ccc tgg cag 336
 Ser Glu Lys Ala Thr Leu Gly Pro Ala Val Arg Pro Leu Pro Trp Gln
 100 105 110

cgc gtg gac cgc gac gtg gca ccg gga act ctc tgc gac gtg gcc ggc 384
 Arg Val Asp Arg Asp Val Ala Pro Gly Thr Leu Cys Asp Val Ala Gly
 115 120 125

tgg ggc ata gtc aac cac gcg ggc cgc cgc ccg gac agc ctg cag cac 432
 Trp Gly Ile Val Asn His Ala Gly Arg Arg Pro Asp Ser Leu Gln His
 130 135 140

gtg ctc ttg cca gtg ctg gac cgc gcc acc tgc aac cgg cgc acg cac 480
 Val Leu Leu Pro Val Leu Asp Arg Ala Thr Cys Asn Arg Arg Thr His
 145 150 155

cac gac ggc gcc atc acc gag cgc ttg atg tgc gcg gag agc aat cgc 528
 His Asp Gly Ala Ile Thr Glu Arg Leu Met Cys Ala Glu Ser Asn Arg
 160 165 170 175

cgg gac agc tgc aag ggt gac tcc ggg ggc ccg ctg gtg tgc ggg ggc 576
 Arg Asp Ser Cys Lys Gly Asp Ser Gly Gly Pro Leu Val Cys Gly Gly
 180 185 190

gtg ctc gag ggc gtg gtc acc tcg ggc tcg cgc gtt tgc ggc aac cgc 624
 Val Leu Glu Gly Val Val Thr Ser Gly Ser Arg Val Cys Gly Asn Arg
 195 200 205

aaag aag ccc ggg atc tac acc cgc gtg gcg agc tat gcg gcc tgg atc 672
 Lys Lys Pro Gly Ile Tyr Thr Arg Val Ala Ser Tyr Ala Ala Trp Ile
 210 215 220

gac agc gtc ctg gcc tagtaggaat tc 699
 Asp Ser Val Leu Ala
 225

<210> 2
 <211> 228
 <212> PRT
 <213> human

<400> 2
 Ile Leu Gly Gly Arg Glu Ala Glu Ala His Ala Arg Pro Tyr Met Ala
 1 5 10 15
 Ser Val Gln Leu Asn Gly Ala His Leu Cys Gly Gly Val Leu Val Ala
 20 25 30
 Glu Gln Trp Val Leu Ser Ala Ala His Cys Leu Glu Asp Ala Ala Asp
 35 40 45
 Gly Lys Val Gln Val Leu Leu Gly Ala His Ser Leu Ser Gln Pro Glu
 50 55 60
 Pro Ser Lys Arg Leu Tyr Asp Val Leu Arg Ala Val Pro His Pro Asp
 65 70 75 80

Ser Gln Pro Asp Thr Ile Asp His Asp Leu Leu Leu Gln Leu Ser
 85 90 95
 Glu Lys Ala Thr Leu Gly Pro Ala Val Arg Pro Leu Pro Trp Gln Arg
 100 105 110
 Val Asp Arg Asp Val Ala Pro Gly Thr Leu Cys Asp Val Ala Gly Trp
 115 120 125
 Gly Ile Val Asn His Ala Gly Arg Arg Pro Asp Ser Leu Gln His Val
 130 135 140
 Leu Leu Pro Val Leu Asp Arg Ala Thr Cys Asn Arg Arg Thr His His
 145 150 155 160
 Asp Gly Ala Ile Thr Glu Arg Leu Met Cys Ala Glu Ser Asn Arg Arg
 165 170 175
 Asp Ser Cys Lys Gly Asp Ser Gly Gly Pro Leu Val Cys Gly Gly Val
 180 185 190
 Leu Glu Gly Val Val Thr Ser Gly Ser Arg Val Cys Gly Asn Arg Lys
 195 200 205
 Lys Pro Gly Ile Tyr Thr Arg Val Ala Ser Tyr Ala Ala Trp Ile Asp
 210 215 220
 Ser Val Leu Ala
 225

<210> 3

<211> 714

<212> DNA

<213> pig

<220>

<221> CDS

<222> (4)...(702)

<400> 3

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 Ile Leu Gly Gly Gln Glu Ala Lys Ser His Glu Arg Pro Tyr Met
 1 5 10 15
 gca tcg gtg cag gtg aac ggc aag cac gtg tgc gga ggc ttc ctg gtg 96
 Ala Ser Val Gln Val Asn Gly Lys His Val Cys Gly Gly Phe Leu Val
 20 25 30
 tct gag cag tgg gtg ctg agt gca gca cac tgc ctg gag gac gtg gcc 144
 Ser Glu Gln Trp Val Leu Ser Ala Ala His Cys Leu Glu Asp Val Ala
 35 40 45
 gag ggg aag ctg cag gtt ctc ctg ggt gcg cac tcc ctg tca cag ccc 192
 Glu Gly Lys Leu Gln Val Leu Leu Gly Ala His Ser Leu Ser Gln Pro
 50 55 60
 gag ccc tcg aag cgc ctg tac gac gtg ctc cgc gcc gtg ccc cac cca 240
 Glu Pro Ser Lys Arg Leu Tyr Asp Val Leu Arg Ala Val Pro His Pro
 65 70 75
 gac agc cag cct gac acc atc gac cat gat ctc ctc ctg ctg aag ctc 288
 Asp Ser Gln Pro Asp Thr Ile Asp His Asp Leu Leu Leu Leu Lys Leu
 80 85 90 95

tcc gag aag gcc gag ctg ggc cct gcc gtg cag ccc ctt gcc tgg caa 336
 Ser Glu Lys Ala Glu Leu Gly Pro Ala Val Gln Pro Leu Ala Trp Gln
 100 105 110

cga gag gac cac gag gtt ccg gca ggc acg ctc tgc gac gtg gcc ggc 384
 Arg Glu Asp His Glu Val Pro Ala Gly Thr Leu Cys Asp Val Ala Gly
 115 120 125

tgg gga gtg gtc agt cac act ggc cgc cgg ccc gac cgt ctg cag cac 432
 Trp Gly Val Val Ser His Thr Gly Arg Arg Pro Asp Arg Leu Gln His
 130 135 140

ctg ctc cta ccg gtg ctg gac cgc acc acc tgc aac ctg cgc aca tac 480
 Leu Leu Leu Pro Val Leu Asp Arg Thr Thr Cys Asn Leu Arg Thr Tyr
 145 150 155

cac gat ggc acc atc acc gag cgc atg atg tgc gcg gag agc aac cgt 528
 His Asp Gly Thr Ile Thr Glu Arg Met Met Cys Ala Glu Ser Asn Arg
 160 165 170 175

cgg gac agc tgc aag ggc gac tcc gga ggc ccg ctg gtg tgc ggg ggt 576
 Arg Asp Ser Cys Lys Gly Asp Ser Gly Gly Pro Leu Val Cys Gly Gly
 180 185 190

gtg gcc gag gga gtg gtt acc tca ggc tcc cga gtc tgc ggc aac cgc 624
 Val Ala Glu Gly Val Val Thr Ser Gly Ser Arg Val Cys Gly Asn Arg
 195 200 205

aag aaa ccc ggc atc tac acg cgc ttg gcg agc tac gtg gcc tgg atc 672
 Lys Lys Pro Gly Ile Tyr Thr Arg Leu Ala Ser Tyr Val Ala Trp Ile
 210 215 220

gag gga gtg atg gct gac agc gca gcc gcc tagtaggaat tc 714
 Asp Gly Val Met Ala Asp Ser Ala Ala Ala
 225 230

<210> 4
 <211> 233
 <212> PRT
 <213> pig

<400> 4

Ile Leu Gly Gly Gln Glu Ala Lys Ser His Glu Arg Pro Tyr Met Ala
 1 5 10 15
 Ser Val Gln Val Asn Gly Lys His Val Cys Gly Gly Phe Leu Val Ser
 20 25 30
 Glu Gln Trp Val Leu Ser Ala Ala His Cys Leu Glu Asp Val Ala Glu
 35 40 45
 Gly Lys Leu Gln Val Leu Leu Gly Ala His Ser Leu Ser Gln Pro Glu
 50 55 60
 Pro Ser Lys Arg Leu Tyr Asp Val Leu Arg Ala Val Pro His Pro Asp
 65 70 75 80
 Ser Gln Pro Asp Thr Ile Asp His Asp Leu Leu Leu Lys Leu Ser
 85 90 95

Glu Lys Ala Glu Leu Gly Pro Ala Val Gln Pro Leu Ala Trp Gln Arg
 100 105 110
 Glu Asp His Glu Val Pro Ala Gly Thr Leu Cys Asp Val Ala Gly Trp
 115 120 125
 Gly Val Val Ser His Thr Gly Arg Arg Pro Asp Arg Leu Gln His Leu
 130 135 140
 Leu Leu Pro Val Leu Asp Arg Thr Thr Cys Asn Leu Arg Thr Tyr His
 145 150 155 160
 Asp Gly Thr Ile Thr Glu Arg Met Met Cys Ala Glu Ser Asn Arg Arg
 165 170 175
 Asp Ser Cys Lys Gly Asp Ser Gly Gly Pro Leu Val Cys Gly Gly Val
 180 185 190
 Ala Glu Gly Val Val Thr Ser Gly Ser Arg Val Cys Gly Asn Arg Lys
 195 200 205
 Lys Pro Gly Ile Tyr Thr Arg Leu Ala Ser Tyr Val Ala Trp Ile Asp
 210 215 220
 Gly Val Met Ala Asp Ser Ala Ala Ala
 225 230

<210> 5
 <211> 25
 <212> DNA
 <213> artificial sequence

<220>
 <223> primer
 <400> 5
 ggccggccgct gtaggtgctg tcttt

25

<210> 6
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> primer
 <400> 6
 ggaattcact cggtattctc gga

23

<210> 7
 <211> 17
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> primer

<400> 7
 tccgagaata acgagtg

17

<210> 8
 <211> 29
 <212> DNA

<213> Artificial Sequence

<220>

<223> primer

<400> 8

cattgaaagc tttgggtag aagttgttc

29

<210> 9

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> primer

<400> 9

cgcgccgca gctgctcaga gtgtaga

27

<210> 10

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> primer

<400> 10

cggttaagctt cactggctca gggaaata

28

<210> 11

<211> 37

<212> DNA

<213> Artificial Sequence

<220>

<223> primer

<400> 11

aagaagcttg ccgccacat ggattggctg tggaact

37

<210> 12

<211> 31

<212> DNA

<213> artificial sequence

<220>

<223> primer

<400> 12

cgggatcctc aaactttctt gtccaccttg g

31

<210> 13

<211> 36

<212> DNA

